



012679-093.ST25

SEQUENCE LISTING

<110> Kim, Sunghoon

<120> Method for Stimulating Wound Healing

<130> 012679-093

<140> US 10/623,567

<141> 2003-07-22

<150> KR 10-2002-42858

<151> 2002-07-22

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 312

<212> PRT

<213> Homo sapiens

<400> 1

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Lys	Glu	Lys	Ala	Ile	Leu	Gln	Ala	Thr	Leu	Arg	Glu	Glu	Lys	Lys	Leu	
		35				40					45					
Arg	Val	Glu	Asn	Ala	Lys	Leu	Lys	Lys	Glu	Ile	Glu	Glu	Leu	Lys	Gln	
	50				55					60						
Glu	Leu	Ile	Gln	Ala	Glu	Ile	Gln	Asn	Gly	Val	Lys	Gln	Ile	Ala	Phe	
65			70					75						80		
Pro	Ser	Gly	Thr	Pro	Leu	His	Ala	Asn	Ser	Met	Val	Ser	Glu	Asn	Val	
			85					90						95		
Ile	Gln	Ser	Thr	Ala	Val	Thr	Thr	Val	Ser	Ser	Gly	Thr	Lys	Glu	Gln	
		100					105					110				
Ile	Lys	Gly	Gly	Thr	Gly	Asp	Glu	Lys	Lys	Ala	Lys	Glu	Lys	Ile	Glu	
		115				120						125				
Lys	Lys	Gly	Glu	Lys	Lys	Glu	Lys	Lys	Gln	Gln	Ser	Ile	Ala	Gly	Ser	
	130				135						140					
Ala	Asp	Ser	Lys	Pro	Ile	Asp	Val	Ser	Arg	Leu	Asp	Leu	Arg	Ile	Gly	
145				150					155						160	
Cys	Ile	Ile	Thr	Ala	Arg	Lys	His	Pro	Asp	Ala	Asp	Ser	Leu	Tyr	Val	
			165					170						175		
Glu	Glu	Val	Asp	Val	Gly	Glu	Ile	Ala	Pro	Arg	Thr	Val	Val	Ser	Gly	
		180					185					190				
Leu	Val	Asn	His	Val	Pro	Leu	Glu	Gln	Met	Gln	Asn	Arg	Met	Val	Ile	
	195					200					205					
Leu	Leu	Cys	Asn	Leu	Lys	Pro	Ala	Lys	Met	Arg	Gly	Val	Leu	Ser	Gln	
	210				215						220					
Ala	Met	Val	Met	Cys	Ala	Ser	Ser	Pro	Glu	Lys	Ile	Glu	Ile	Leu	Ala	
225				230					235						240	
Pro	Pro	Asn	Gly	Ser	Val	Pro	Gly	Asp	Arg	Ile	Thr	Phe	Asp	Ala	Phe	
			245					250						255		
Pro	Gly	Glu	Pro	Asp	Lys	Glu	Leu	Asn	Pro	Lys	Lys	Lys	Ile	Trp	Glu	
		260					265						270			

. 012679-093.ST25

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Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
      275      280      285
Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
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Thr Met Ser Asn Ser Gly Ile Lys
305      310

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<210> 2
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe for Southern blot

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<400> 2
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<210> 3
 <211> 1226
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe for Southern blot

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68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 646, 647,
648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659,
660, 661, 662, 663, 1212, 1213, 1214, 1215, 1216, 1217
<223> n = A,T,C or G

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<221> misc_feature
<222> 1218, 1219, 1220, 1221
<223> n = A,T,C or G

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<400> 3
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aatgtgtgtg tgccctgcatt tgtgtgtatg caccattgcg tgcatacctg gagcctgcag 180
aggctagaag aggggttcaa cctggaactg aggctacagg tggttgttga gtatccacat 240
agatgctcgg aattaaacct gggttctcca gtccaagga gactaaatat tttcaaagta 300
agcctgcact ttgtactaca gtaaaataaa accactgtgg agtgactaat ataaaatagt 360
aagatgagct ctagattaac aggcaaaagt ttaagttttc agtattgtta aagtagcacc 420
atctccctaa agagaacccat atttattttc cttccagtct tctgtgtttc cctcttttgt 480
ttgaaagttt agtgagtgtt tatttttctt actgtgaaca caacatgaga caaactcagg 540
gattgtaaga gatcatggac ataaattact tttaggaacc tggcactcaa atgaaaatta 600
attagtgaca agttggcatg gcattttatt attaaccctg ggtggnnnnnn nnnnnnnnnn 660
nnntaaactg cgtgggtgatg atttgtgatt gcaagaagac atagatatga agctctgaac 720
aacagtgtcc aggcaacatg tgaagaaaag gccctatgga ggggcaggag agcagggtgag 780
agcatcctaa tagaaattca gacagtgaag caagaagttg ttcacacagc ccacacagcc 840
tgtaagtgtt tcttcaacta aggtttgttg actgtaacca ctttttctaa agaaaacatt 900
aagaaaaaca taggtgtctg ttcgcttcct atttgcgtct gtgattaaaa cgctgaccaa 960
aagcaacttg gctgaggagc cgtttttgta tttctccgtt taggtagcaa tgaagttgga 1020
gcaggaggaa ggggtgcttac aggctagctc tcctgctctc cttgagcaag cattcttgtg 1080
gtagctcagg actccctgca cagtgcacac ccacgtgctt cttcaggggg acttcaaact 1140

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actgtacacc ctttccttct gtcgaccata tgggagagct cccaacgcgt tggatgcata 1200
gcttgagtat tnnnnnnnnn nagctt 1226

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> IF3 primer for PCR

<400> 4 30
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<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> IR3 primer for PCR

<400> 5 27
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<210> 6
<211> 31
<212> DNA
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<220>
<223> pKOF2 primer for PCR

<400> 6 31
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<210> 7
<211> 838
<212> DNA
<213> Artificial Sequence

<220>
<223> p43-specific probe for Northern blot

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caggttgctc ttcttaagga gaaagcaatt ttgcaggcaa caatgagaga agaaaaagaaa 180
cttcgagttg aaaatgctaa actgaaaaaa gaaatagaag agctaaagca agagctgatt 240
ctggcagaaa ttcataacgg agtggagcaa gtgcgtgttc gattgagtac tccactgcag 300
acgaactgta ctgcttctga aagtgtggtg cagtctccat cagtagcaac caccgcctct 360
cctgctacaa aagagcagat caaagcggga gaagaaaaga aggtgaaaga gaagactgaa 420
aagaaaggag agaaaaagga gaagcagcag tcggcagcag caagtactga ctccaagcct 480
atcgacgcat cgcgtctgga tcttcgaatt gggtgtattg ttactgccaa gaagcaccct 540
gatgcagatt cactgtatgt ggaggaagta gatgtgggag aagcagcccc gcgcacggtc 600
gtcagcgggc tggatgaatca tgttcctcta gaacagatgc aaaatcgtat ggtgggttta 660
ctctgtaatc tgaagcctgc aaagatgcgg ggagttctgt ctcaagccat ggtgatgtgt 720
gccagttcac cagagaaagt ggagattctg gccctccca acgggtccgt tcctggggac 780
agaattactt ttgatgcttt tcctggagag cctgacaagg agctaaaccc taagaaga 838